

**IN THE SPECIFICATION:**

On p. 2, l. 16, delete: "is required".

On p. 6, l. 23, replace the blank with the Division of Biological Sciences for the University of Missouri".

**IN THE CLAIMS:**

1. (Amended) A computer-implemented method for identifying relative binding motifs of peptide-like molecules, comprising the steps of:

- (a) training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptide-like molecules, each of known sequence and binding affinity;
- (b) applying to the ANN input data characterizing at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
- (c) analyzing each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and outputting such prediction.

(Amended) A computer-implemented method for identifying relative peptide binding motifs, comprising the steps of:

- (a) training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (b) applying to the ANN input data characterizing at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (c) analyzing each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and outputting such prediction.

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4  
3  
(Amended) The method of claim ~~2~~ 3, wherein the set of training peptides include peptides having a binding affinity for [MHC] major histocompatibility complex (MHC) class I molecules.

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(Reiterated) The method of claim ~~3~~ 3, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.

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2  
(Reiterated) The method of claim ~~2~~ 2, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

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(Reiterated) The method of claim ~~5~~ 5, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.

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12  
(Reiterated) The method of claims 1 or ~~2~~ 2, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

8. A computer-implemented system for identifying relative binding motifs for peptide-like molecules, comprising:

- (a) means for training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptide-like molecules, each of known sequence and binding affinity;
- (b) means for applying to the ANN input data characterizing at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
- (c) means for analyzing each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and output such prediction.

A computer-implemented system for identifying relative peptide binding motifs, comprising:

- (a) means for training [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (b) means for applying to the ANN input data characterizing at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (c) means for analyzing each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and output such prediction.

(*Reiterated*) The system of claims 8 or ~~9~~, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

15. (Amended) A computer program, residing on a computer-readable medium, for identifying relative binding motifs for peptide-like molecules, comprising instructions for causing a computer to:

- (a) train [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptide-like molecules, each of known sequence and binding affinity;
- (b) apply to the ANN input data characterizing at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
- (c) analyze each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and output such prediction.

(Amended) A computer program, residing on a computer-readable medium, for identifying relative peptide binding motifs, comprising instructions for causing a computer to:

- (a) train [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (b) apply to the ANN input data characterizing at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
- (c) analyze each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and output such prediction.

~~17~~  
~~17~~ (Amended) The computer program of claim ~~16~~<sup>16</sup>, wherein the set of training peptides having a binding affinity for [MHC] major histocompatibility complex (MHC) class I molecules.

~~18~~  
~~18~~ (Reiterated) The computer program of claim ~~17~~<sup>17</sup>, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.

~~19~~  
~~19~~ (Reiterated) The computer program of claim ~~18~~<sup>18</sup>, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

~~20~~  
~~20~~ (Reiterated) The computer program of claim ~~19~~<sup>19</sup>, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.

~~21~~  
~~21~~ (Reiterated) The computer program of claims 15 or ~~16~~<sup>17</sup>, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

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